GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nuc	arch, using sw model
Run on:	January 7, 2004, 04:41:34 ; Search time 23414 Seconds (without alignments) 11736.139 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-082-272-1 6717 1 gcgccgcgctccccacgccataaaaaaaaaaaaa
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 seqs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seg ] Maximum DB seg ]	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:*  1: gb_ba:* 2: gb_htg:* 3: gb_ntg:* 4: gb_om:* 5: gb_ov:* 6: gb_pb:* 7: gb_ph:* 9: gb_pp:* 10: gb_r:* 11: gb_sts:* 11: gb_sts:* 11: gb_sts:* 12: gb_un:* 13: gb_un:* 14: gb_vi:* 15: em_hum:* 16: em_hum:* 17: em_nu:* 18: em_in:* 19: em_ov:* 22: em_ov:* 23: em_ov:* 24: em_ph:* 25: em_ph:* 26: em_ph:* 27: em_sts:*

em_un:*	em_v1:*	em_htg_hum:*	em_htg_inv:*	em htg_other:*	em_htg_mus:*	em_htg_pln:*	em_htg_rod:*	em_htg_mam:*	em_htg_vrt:*	em_sy:*	em_htgo_hum:*	em_htgo_mus:*	em_htgo_other:*
28:	29:	30:	31:	32:	33:	34:	35:	36:	37:	38:	39:	40:	41:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
Res	Result No.	Score	f Query Match	Length	DB	CI	Description
U	-		78.0		0	AC005826	AC005826 Homo sapi
υ	7	5203.8	77.5	202719	σ	AC006379	AC006379 Homo sapi
	m	4812.4	71.6	188527	σ	AC084357	AC084357 Homo sapi
υ	4	3623.4	53.9	189515	7	AC026105	AC026105 Homo sapi
υ	Ŋ	3350.8	49.9	150207	7	AL451067	AL451067 Homo sapi
U	9	3287.6	48.9	187651	7	AC055122	AC055122 Homo sapi
	7	3275	48.8	173398	7	AC092972	AC092972 Homo sapi
	00	1554.2	23.1	3999	10	AF306667	AF306667 Mus muscu
	σ	1388	20.7	187651	7	AC055122	Homo
	10	973.2	14.5	150207	7	AL451067	
	11	947	14.1	1082	9	AR220868	Seque
	12	916.8	13.6	1323	Ŋ	AB070554	AB070554 Gallus ga
	13	831.8	12.4	1741	ហ	AY154394	AY154394 Xenopus l
	14	796.6	11.9	1826	10	AF260557	7
	15	782	11.6	2105	Ŋ	AF239664	AF239664 Danio rer
	16	769.2	11.5	2134	Ŋ	AF253325	AF253325 Danio rer
υ	17	765.6		246543	N	AC097034	AC097034 Rattus no
	18	734.8	10.9	982	10	MMU277486	AJ277486 Mus muscu
	13	633.8	9.4	900	9	BD017880	
	20	633.8	9.4	900	9	BD097818	BD097818 Novel gen
υ	21	614.8	9.5	892	9	BD017881	Novel
υ	22	614.8	9.2	892	9	BD097819	BD097819 Novel gen
	23	602	9.0	602	σ	HSA237589	AJ237589 Homo sapi
υ	24	587.4	8.7	168799	σ	AC009531	1 Homo
υ	25	409	6.1	482	11	G36805	SHGC-
υ	56	389.4	8	486	9	BD110970	BD110970 EST and e
	27	378.4	5.6	154865	σι	AC099757	AC099757 Homo sapi
υ	28	378.4	5.6	163314	(A	AL590557	ALS90557 Homo sapi
	59	272	4.0	198463	σ	AL353683	AL353683 Human DNA
	30	268.6	4.0	152695.	N	AC142204	AC142204 Homo sapi
	31	268.6	4.0	205619	N	AC133567	AC133567 Homo sapi
υ	32	268.6	4.0		(1	AC142200	AC142200 Homo sapi
	33	266.8	4.0	3155	n	DMY16899	Y16899 Drosophila

AC008006 Homo sapi	AC092375 Homo sapi	AC145137 Homo sapi	AC023629 Homo sapi	AC145130 Homo sapi	AC079767 Homo sapi	AC138995 Homo sapi	AL122004 Human DNA	AC010331 Homo sapi	AC106788 Homo sapi	AF001549 Human Chr	AC132806 Homo sapi
AC008006	AC092375	AC145137	AC023629	AC145130	AC079767	AC138995	HSJ678E16	AC010331	AC106788	HUAF001549	AC132806
6	σ	7	7	(1	σ	7	σ	σ	σ	σ	7
164076	173275	166628	188076	197752	90606	148012	3.9 107037 9 H	114491	170613	202004	167672
4.0	4.0	9. 6.	9.9	3.9	9.9	3.9	9.9	3.9	3.9	3.9	6.6
266.2							263.8				262.4
34	35	36	37	38	39	40	4.7	42	43	44	45
	υ		υ	U	υ			υ	υ		υ

Search completed: January 7, 2004, 17:54:50 Job time : 23479 secs

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OM nucleic - nucleic search, using sw model

Run on:	January 7, 2004, 04:37:20 ; Search time 1564 Seconds (without alignments) 11593.430 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-082-272-1 6717 1 gcgccgcgctccccacgccataaaaaaaaaaaaa
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2552756 seqs, 1349719017 residues
Total number of	Total number of hits satisfying chosen parameters: 5105512
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 0%

6717						
ааааааааааааааа			5105512			-embl/NA1980.DAT: -embl/NA1982.DAT: -embl/NA1982.DAT: -embl/NA1983.DAT: -embl/NA1983.DAT: -embl/NA1986.DAT: -embl/NA1986.DAT: -embl/NA1986.DAT: -embl/NA1987.DAT: -embl/NA1987.DAT:
6717 1 gcgccgcgctccccacgccataaaaaaaaaaaaa	xt 1.0	9719017 residues	Total number of hits satisfying chosen parameters:		O% summaries	19Jun03:* SIDS1/gcgdata/geneseqn.embl/NA1980.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1981.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1984.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1986.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1986.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1986.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1987.DAT:* SIDS1/gcgdata/geneseq/geneseqn.embl/NA1987.DAT:*
6717 l gegeegeteeea	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	2552756 segs, 1349719017 residues	nts satisfying c	ngth: 0 ingth: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_19Jun03:* 1: /SIDSI/gcgdata/g2 2: /SIDSI/gcgdata/g4 4: /SIDSI/gcgdata/g4 5: /SIDSI/gcgdata/g5 5: /SIDSI/gcgdata/g7 6: /SIDSI/gcgdata/g7 7: /SIDSI/gcgdata/g7 8: /SIDSI/gcgdata/g7 8: /SIDSI/gcgdata/g7 9: /SIDSI/gcgdata/g7 10. /SIDSI/gcgdata/g7 11. /SIDSI/gcgdata/g7 11. /SIDSI/gcgdata/g7 11. /SIDSI/gcgdata/g7 11. /SIDSI/gcgdata/g7 11. /SIDSI/gcgdata/g7
Perfect score: 6 Sequence: 1	Scoring table: I	Searched: 2	Total number of h	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 10 Listing first 45	Database : 2 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4

/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* /SIDS1/gcgdata/geneseqn-embl/NA1991.DAT:*	/SIDS1/gcgdarc/gcneseq/gcneseqn.embl/NA1993.DAT:* /SIDS1/gccdara/geneseq/geneseqn.embl/NA1993.DAT:*	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*	/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*/SIDS1/qcqdata/geneseq/geneseqn-emb1/NA1998.DAT:*	/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*/SIDS1/gcgdata/geneseg/geneseqn-embl/NA2000.DAT:*	/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*	/azozigugatak/gunesey/gunesey/azoziz: DSDSI/gogdata/geneseq/genesegn-emb1/NA202.DAT:* /SIDSI/gogdata/geneseq/genesegn-emb1/NA2003.DAT:*
/geneseq/genes/ /geneseq/genes/	/geneseq/genes /geneseq/genes	/geneseq/genes/	/geneseq/genes	/geneseq/genes /geneseq/genes	/geneseq/genes	/geneseq/genes/
/SIDS1/gcgdata /SIDS1/gcgdata	/SIDS1/gcgdata /SIDS1/gcgdata	/SIDS1/gcgdata /SIDS1/gcgdata	/SIDS1/gcgdata /SIDS1/gcgdata	/SIDS1/gcgdata /SIDS1/gcgdata	/SIDS1/gcgdata	/SIDS1/gcgdata /SIDS1/gcgdata /SIDS1/gcgdata
11:	14:	16:	18:	20:	22:	24:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Human bone remodel	Novel human cDNA s	Human neuroblastom	Human neuroblastom	Human cDNA encodin	Human DNA #1 co-ex	Drosophila melanog	Human immune/haema	Human immune/haema	Human immune/haema	Human cDNA differe	Human immune/haema	Human immune/haema	Human immune/haema	Human immune/haema	Human atrionatriur	Human immune/haema	Genomic sequence #	Human digestive sy	Human digestive sy	-	Genomic DNA #171 e	Human immune/haema	Human immune/haema	Human immune/haema	Human prostate exp	Human prostate exp	Human immune/haema	Human immune/haema	cDNA encoding huma	Human osteoblast d	Human immune/haema
		9	ABS70452	ABX70833	AA194043	AAI94044	AAS34058	AAD42842	ABL17451	AAK67293	AAK74865	AAK83153	ABK83461	AAK74878	AAK83177	AAK83210	AAK83183	AAS16995	AAK83152	AAS39620	AAK89019	AAK91533	AA157790	ABS99967	AAK74867	AAK83217	AAK74877	ABV23884	ABV29765	AAK71948	AAK82518	ABK88014	ABQ88177	AAK83220
		DB	24	25	22	22	22	24	23	22	22	22	24	22	22	22	22	24	22	22	22	22	22	24	22	22	22	23	23	22	22	24	24	22
		Length	1082	1143	900	892	631	790	2100	31405	31405	31405	128600	21332	21332	14258	14260	15810	15364	32204	32204	32204	32204	32204	21621	14260	24102	3772	3772	3128	34831	2637	125439	15772
dР	Query	Match	14.1	12.5	•	9.5	8.0	5.7	4.0	3.9	3.9	3.9	3.9	3.8	3.8	3.8	3.8	3.8		3.8	3.8	3.8	3.8	3. 8.		3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7
		Score	947	841	633.8	614.8	540.2	385.8	268.4	263	263	263	259.6	258.4	258.4	258.2	258.2	256.2	255.4	253.2	253.2	253.2	253.2	253.2	S	251.8	251.8	251.4	S	250.8	LO.	250.4	50.	250
	ult	No.	7	7	m	4	ιO	9	7	00	9	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	53	30	31	32
	Resul					υ				U										υ	υ									υ			υ	

Human neuregulin 1	Human neuregulin 1	Human neuregulin-1	Human neuregulin-1	Human immune/haema	Secreted protein g	Human PPMIG serine	Human DNA for a no	Human osteoblast d	Human immune/haema	Human immune/haema	Ovary cancer relat	Human multidrug re
ABT00010	ABT01503	AAK95240	AAK96733	AAK83105	AB274497	3.7 29695 24 ABQ78853	AAS34624	ABQ88143	AAK83173	AAK83209	ABL68122	ABS98441
24	24	22	22	22	25	24	22	24	22	22	24	24
1503841	1503841	1503900	1503900	6547	6547	29692	27289	121724	18488	13774	174424	28123
3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7
250	250	250	250	249.6	249.6	249.6	249.4	249.2	249	248.6	248.6	248.4
33	34	35	36	37	38	33	40	41	42	43	44	45
υ	U	υ	υ	υ			υ	υ				υ

Search completed: January 7, 2004, 11:23:28 Job time : 1581 secs GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

1

OM nucleic - nucleic search, using sw model

Run on:	January 7, 2004, 09:48:03 ; Search time 12380 Seconds (without alignments) 13186.847 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-082-272-1. 6717 1 gcgccgcgctccccacgccataaaaaaaaaaaaaa
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	22781392 segs, 12152238056 residues
Total number of	Total number of hits satisfying chosen parameters: 45562784
Minimum DB seq length: 0 Maximum DB seq length: 2	seq length: 0 seq length: 200000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	EST:*  1. em_estba:*  2. em_esthum:*  3. em_estin:*  5. em_estro:*  6. em_estpl:*  7. em_estro:*  8. em_htc:*

gb_est2:*	gb_htc:*	gb_est3:*	gb_est4:*		em_estfun:*	em_estom:*	em gss inv:*	em_gss_pln:*	em_gss_vrt:*	em_gss_fun:*	em gss mam:*		em gss pro:*		em_gss_phg:*		1	
10:	11:	5:	 m	4:	 S		 			::	22:	23:	24:	25:	26:	27:	28:	29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.   Score   Match   Length   DB   ID				,			SUMMARIES	
No. Score Match Length DB ID  2 798.2 11.9 3487 11 AK052185 2 649.4 9.7 13 BX324356 5 519.2 7.0 47.0 13 BX324356 6 519.2 7.0 697 13 BX324356 6 519.2 7.0 697 13 BX324356 8 468 7.0 552 2 H8N092075 9 462.8 6.9 466 9 AA937310 11 425.6 6.3 466 9 AA937310 12 40.9 6.1 411 9 AA960800 13 40.9 6.1 411 9 AA960800 13 40.9 6.1 411 9 AA960800 14 398.2 5.7 649 14 BB652125 15 385 5.7 649 14 BB652125 16 343 5.1 549 12 BP109070 18 343 5.1 549 12 BP109070 19 341 5.1 456 14 BE046007 19 343 5.1 456 14 BE046007 10 338 5.0 338 9 AZ07046 11 39.3 5.0 348 9 AA700765 12 3308.8 4.6 600 BB662398 12 308.8 4.6 600 BB662398 12 308.8 4.6 600 BB662398 12 55.2 3.8 67 10 BB662398 12 BB662328 13 BB662338 14 39.3 5.0 369 10 BB662398 15 BB666328 16 BB665338 17 55.0 389 10 BB662398 18 BB665338 18 BB6653345 18 BB6653345 18 BB6653345 18 BB6653345 18 BB6653345 18 BB665345 18 BB6653345 18 BB6653345 18 BB6653345 18 BB6653345 18 BB665345 18 BB665346	Resn	ilt		* Query				
1516.8   22.6   4026   11   AKO52389   AKO52389   AKO52389   2	2	. 6	Score	Match	Length	88	ΙD	Description
2         798.2         11.9         3487         11         AKO52155         AKO52155         AKO52155         34         65.65.2         BX38215         BX38215         BX38215         BX382156         BX382166         BX3821666         BX382166         BX		-	1516.8	22.6	4026	11	AK052389	AK052389 Mus muscu
3         677         10.1         901         13         BQ216652         BQ216652         BQ216652         BQ216652         BX388215         BX389215         BX389215         BX389215         BX3891200         BX399212         BX399212         BX39921310         BX39921310         BX399212         BX39921310         BX3992125         BX399229         BX3992125         BX3992125		4	798.2	11.9	3487	11	AK052155	AK052155 Mus muscu
4         652.6         9.7         969         13         BX388215         BX388215           5         649.4         9.7         697         13         BX324256         BX24366           5         12.2         7.7         536         2         HSW09229         BX243612           7         472.2         7.0         477         9         A1936589         A1936589         A1936589           8         468         6.9         466         9         AA937710         A1936589         A19365812           10         435.6         6.5         575         12         BM087995         BX498612         A19365812           11         425         6.3         425         9         AA937710         AA96080         BM087995           12         401         10         BM087995         AA96080         AA96080         AA96080         AA96080           13         403         6.1         10         BM652125         BM087995         AA96080         AA96080         AA96080           14         393.2         5.9         641         10         BM652125         BB652125         BB652125         BB652125         BB700070         AA96080         AA96080		m	677	10.1	901	13	BQ216652	BQ216652 AGENCOURT
5         649.4         9.7         697         13         BX324356         BX324356           6         519.2         7.7         536         2         HSM092559         AX90542         AX905542         AX905434         AX90544         AX90644         AX906444         AX90644         AX906444         AX906444		4	652.6	7.6	696	13	BX388215	BX388215 BX388215
6         519.2         7.7         536         2         HSM095c259         AF502542 H           7         472.2         7.0         47.7         9         468.9         9         AA937310         Bx498612 H           10         452.6         6.9         466         9         AA937310         Bx498612 H         AA937310 O           11         425         6.3         452         9         AA937310         BM087995           11         425         6.3         428         AR80884         AR96080         AR96080           13         409         6.1         411         AA96080         AA96080         AA96080           13         409         6.1         482         14         N93760         AA96080         AA96080           14         393.2         5.9         641         10         BE65125         BB665125         BB665125           15         385         5.7         649         14         CB441644         CB441644         CB441644           16         366         5.4         366         10         BE046007         BB066007         BB066007           17         353         5.1         461         1		ß	649.4	7.6	697	13	BX324356	BX324356 BX324356
7         472.2         7.0         477         9         A1936589         A19365812         A193612         A193612         A1937310         <		9	519.2	7.7	536	۲3	HSM096259	Ex502542 Homo sapi
8         468         7.0         552         2         HSM092075         Bx498612         H           9         46.2.6         6.9         466         9         AA937310         AA937310         BM087952         BM087952         BM087952         AA937310         BM087952         BM087952         BM087952         BM087952         BM087954         AA906880         AA906880         AA906880         AA966800         AA96660         AA966800         AA966800         AA966800         AA966800         AA96660         AA966800	υ	7	472.2	7.0	477	σ	AI936589	A1936589 wd29g06.x
9         465.8         6.9         466         9         AA937310         AA937310           10         425.6         6.5         575         12         BM087995         BM087995           11         421         6.1         411         9         AA960804         AA960809           13         409         6.1         442         14         M93760         M94700         M9470		ω	468	7.0	552	7	HSM092075	
10   435.6   6.5   575   12   BM087995   BM087995   BM087995   11   425   6.3   426   425   6.3   426   42	υ	6	462.8		466	δ	AA937310	AA937310 om16h09.s
11   425   6.3   425   9 A.808884   A.808888   A.8088		10	435.6		575	12	BM087995	BM087995 501340 MA
12         411         6.1         411         9         AA960800         AA960800           13         409         6.1         441         10         BB652125         BB652125         BB652125         BB652125         BB652125         BB652125         BB652125         BB652125         BB6652125         BB6652125         BB6652125         BB6652125         BB6652125         BB6652125         BB6652125         BB6652125         BB6641644         BB641644         BB641664         BB641644	υ	1	425		425	σ	AI808884	AI808884 wf66a05.x
13         409         6.1         482         14         N93760         N93760 zb           14         393.2         5.9         641         10         BB652125         BB652125           16         365         5.4         366         10         BE646007         BE641644         CB441644           17         353         5.3         384         9         AA700765         AA700765         AA700766           18         343         5.1         2840070         BP109070         BP109070         BP109070           19         341         5.1         456         12         BE049094         AA700766         AA700766           20         333.6         5.0         369         10         BE049094         AI207046         AI207046           21         333         5.0         33         9         AA2081683         BE049094           22         319         4.6         600         28         AQ681683         AD681683           23         308.8         4.6         600         28         AQ681683         BB480212           24         306.8         4.6         638         10         BB662398         BB662398	υ	12	411	6.1	411	6	AA960800	AA960800 on96h02.s
14         393.2         5.9         641         10         BB652125         BB652125           15         385         5.7         649         14         CB441644         CB44164           16         366         5.7         649         14         DB441644         CB441644           17         353         5.3         384         9         AA700765         BB046007           18         343         5.1         549         12         BP109070         BP109070           20         33.4         5.1         549         12         BD40913         RO2483         RO2483           21         33.6         5.0         369         10         BE0449094         BD408070           21         33.3         5.0         33.3         9         AZ20746         AZ207046           22         319         4.7         458         13         BY385297         BY385297           24         306.8         4.6         600         28         AQ6816633         BB480212           25         30.2         4.5         396         10         BB662398         BB662398           27         255.7         3.8         67         <	υ	13	409	6.1	482	14	N93760	N93760 zb64c01.s1
15         385         5.7         649         14         CB441644         CB441644           16         366         5.4         366         10         BE046007         BE046007           18         343         5.1         549         12         BP109070         BP109070           19         341         5.1         545         14         RA2403         BP109070           21         333         5.0         369         10         BE049094         BE049094           22         333         5.0         333         9         AI207046         BY385297           23         308.8         4.6         600         BA681633         BB480212           24         306.8         4.6         638         10         BB480212         BB662398           25         302.8         4.5         396         10         BB662398         BB662398           27         255.2         3.8         67         10         BB65345         BB65348		14	σ	5.9 .9	641	10	BB652125	BB652125 BB652125
16         366         S.4         366         10         BE046007         BE046007           17         353         S.3         384         9         AA700765         BA700765         BA700765         BA700766         BA700766         BA700766         BA700766         BA700766         AA700766         AA7007676         AA700766         AA700766         AA70		15	385	5.7	649	14	CB441644	CB441644 692147 MA
17         353         5.3         384         9         AA700765         AA700765         AA700765         AA700765         2           18         343         5.1         549         12         BEL09070         BPL09070         BPL09070         BPL09070         BPL09070         BPL09070         BPL09070         BPL09070         BPL08070         BPL08070 <td>υ</td> <td>16</td> <td>366</td> <td>5.4</td> <td>366</td> <td>10</td> <td>BE046007</td> <td>BE046007 hd91e03.x</td>	υ	16	366	5.4	366	10	BE046007	BE046007 hd91e03.x
18         343         5.1         549         12         BP109070           19         341         5.1         456         14         R02463         BP109070           20         33.6         5.0         369         10         BE0449094         BE0449094           21         33.3         5.0         33.3         9         AI207046         AI207046         AI207046           22         31.9         4.7         458         13         BY382297         BY385297           24         306.8         4.6         60         28         AG681633         AB681633           25         302.8         4.6         638         10         BB460212         BB6480212           25         302.8         4.5         396         10         BB662398         BB6480212           27         255.7         3.8         667         10         BB653345         BB653345		17	353	5.3	384	σ	AA700765	AA700765 zi66a02.s
19         341         5.1         456         14         R02483         R02483 ye           20         33.6         5.0         369         10         BE049094         BE04904           21         33.3         5.0         35.9         10         BE049094         BE04904           22         31.9         4.7         458         13         BY382297         BY3878297         BY3878297           23         308.8         4.6         600         28         AQ681683         AQ681683           24         306.8         4.6         638         10         BB468212         BB480212           25         302.8         4.5         536         10         BB652398         BB652398           27         255.2         3.8         667         10         BB65345         BB65345	υ	78	343	5.1	549	12	BP109070	BP109070 BP109070
20         333.6         5.0         369         10         BE049094         BE049094           21         333         9         AZ007046         AI207046         AI207046           22         319         4.7         4583         AZ007046         AZ007046           23         308.8         4.6         600         28         AQ681683         AQ681683           24         306.8         4.6         638         10         BB480212         BB480212           25         302.8         4.5         396         10         BB662398         BB662398           27         255.2         3.8         667         10         BB65345         BB65345	υ	49	341	5.1	456	14	R02483	R02483 ye86c03.rl
21         333         5.0         333         9         AI207046         AI207046         AI207046           22         319         4.7         458         13         BY385297         BY385297           23         308.8         4.6         600         28         AQ681663         AQ681663           24         306.8         4.6         638         10         BB480212         BB480212           25         302.8         4.5         396         10         BB662398         BB662398           27         255.7         3.8         667         10         BB65345         BB659345	U	20	333.6	5.0	369	10	BE049094	BE049094 xr72a06.x
22     319     4.7     458     13     BY385297     BY385297       23     308.8     4.6     600     28     AQ681683     AQ681663       24     306.8     4.6     638     10     BB480212     BB480212       25     302.8     4.5     396     10     BB662398     BB662398       27     255.2     3.8     667     10     BB659345     BB659345	υ	21	333		333	0	A1207046	A1207046 qf80c08.x
23 308.8 4.6 600 28 AQ681683 AQ681683 24 306.8 4.6 638 10 BB4680212 25 302.8 4.5 636 10 BB659398 BB652398 27 255.2 3.8 667 10 BB659345 BB659345		22	319		458	13	BY385297	BY385297 BY385297
4 36.8 4.6 638 10 BB480212 BB480212 5 302.8 4.5 396 10 BB662398 BB662398 6 296 4.4 668 13 BU358229 BU358229 7 255.2 3.8 667 10 BB659345 BB659345	υ	23	308.8	4.6	900	28	AQ681683	AQ681683 HS_2161_A
5 302.8 4.5 396 10 BB662398 BB662398 6 296 4.4 686 13 BU358229  BU358229 7 255.2 3.8 667 10 BB659345 BB659345		24	306.8	4.6	638	10	BB480212	
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7 255.2 3.8 667 10 BB659345 BB659345			296		æ	13	BU358229	BU358229 603479159
		27	55	3,00		10	5934	934

BG739841 602630570	Bx480803 Homo sapi	BC017002 Homo sapi	AQ489530 RPCI-11-2	AG153670 Pan trogl	Bx482633 Homo sapi	CA434553 UI-H-DH0-	AQ386056 RPCI11-14	AU147922 AU147922	AQ385524 RPCI11-14	BM989011 UI-H-DF0-	BM919569 AGENCOURT	BM310229 ih09f10.x	AQ219156 HS_3253_B	B75932 RPCI11-12N1	AG185221 Pan trogl	AQ787773 HS 3072 A	BG391274 602417318
BG739841	HSM070969	BC017002	AQ489530	AG153670	HSM072801		AQ386056	AU147922	AQ385524	BM989011	BM919569	BM310229	AQ219156	B75932	AG185221	AQ787773	BG391274
10	C)	11	78	59	7	14	58	σ	28	12	12	12	28	28	53	28	10
544	339	1374	298	667	663	605	769	493	582	625	1043	549	488	469	790	894	383
3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6
250.8	248.4	248.4	247.8	247.8	247.4	246	246	245.8	245.4	244.8	244.2	243.8	243.2	243	243	242.6	242.2
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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